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MIPR NUMBER 93MM3506

TITLE: Interphase Cytogenetics in Breast Tumors P53 Gene Alterations

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REPORT DATE: October 1993

TYPE OF REPORT: Midterm

PREPARED FOR: U.S. Army Medical Research and Materiel Command Fort Detrick, Maryland 21702-5012

DISTRIBUTION STATEMENT: Approved for public release; distribution unlimited

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19980423 030

REPORT DOCUMENTATION PAGE			Form Approved OMB No. 0704-0188
Public reporting hundern for this collection of information soldnesses and maintaining the data needed, and complet collection of information, installing suggestions for read- Darie Highway, Suits 1204, Arlington, VA 22202-436.	is estimated to everage 1 hour per si ling and reviewing the eatherlien of in sing this burden, to Washington Hood 2, and to the Office of Management of		o for exclusing instructions, exercising exterior data sources, a respecting the human estimate or any other expect of this main for this except the department and futures, 1215 Justices, dentice from the 4-5168, Washington, DC 20682.
1. AGENCY USE ONLY (Leeve blank)	2. REPORT DATE October 1993	3. REPORT TY Midteen (27	PE AND DATES COVERED Oct 92 - 30 Sep 93)
4. TITLE AND SUBTITLE Interphase Cytogenetics in Breast Tur	5. FUNDING NUMBERS 93MM3506		
S. AUTHOR(S) Sesterhenn, Isabell A, M.D.	·		
7. PERFORMING ORGANIZATION NAME: Armed Forces Institute of Pathology Washington, DC 20306-6000	8. PERFORMING ORGANIZATION REPORT NUMBER		
9. SPONSORING / MONITORING AGENCY U.S. Army Medical Research and Ma Fort Detrick, Maryland 21702-5012		(ES)	10.SPONSORING / MONITORING AGENCY REPORT NUMBER
1. SUPPLEMENTARY NOTES			
2a. DISTRIBUTION / AVAILABILITY STA	TEMENT		12b. DISTRIBUTION CODE
Approved for public release; distributi	on unlimited		
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13/21, 17, and X. However, in individual cases, loss of chromosome 17 and X

chromosome was encountered.

14. SUBJECT TERMS

Breast Cancer

15. NUMBER OF PAGES

16. PRICE CODE

17. SECURITY CLASSIFICATION OF THIS PAGE

Unclassified

19. SECURITY CLASSIFICATION OF ABSTRACT

Unclassified

Unclassified

Unclassified

Unclassified

Unclassified

Unclassified

Unclassified

in nuclear grade I, II, and III tumors. Comparison of copy numbers of the different chromosomes in tumor to normal epithelial cells showed a gain for chromosomes 8, 11,

FOREWORD

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MID-TERM REPORT - 93MM3506

TITLE OF PROPOSAL: Interphase Cytogenetics in Breast Tumors p53 Gene Alterations.

PRINCIPAL INVESTIGATOR: Isabell A. Sesterhenn, M.D.

Ref.: DD Form 448, Amendment received [dated 12/10/96] extending proposal period until 30 JUNE 1998.

PURPOSE: To compare numerical chromosome aberrations and p53 gene alterations in 250 node-negative breast cancers to 250 non-positive breast cancers and their survival. Although conventional cytogenetic analysis has been successful only in about 50 breast cancers, it has been helpful in identification of subtypes of ductal carcinomas. Since cytogenetic equivalents for gene amplification are net gain of chromosomal material and for loss of heterozygosity are net loss of chromosomal material or structural aberrations, we believe that interphase cytogenetics may be helpful in subclassification of ductal carcinomas. P53 gene alterations may prove to be an early event in breast cancer progression.

SCOPE: Interphase cytogenetics will be performed in paraffin sections utilizing biotinylated probes specific for centromeric regions of chromosomes 1, 8, 11, 13, 17, 18, and X. - Chromosome profiles based on 300 tumor cells will be generated for each patient. Serial sections of the same paraffin blocks will be utilized by Dr. O'Leary to assess p53 alterations immunohistochemically. If present, further amplification and sequencing of p53 gene will be done utilizing PCR denaturing gel gradient electrophoresis and coupled amplification and sequencing protocols. The data will be analyzed by the Kaplan-Meyer and Cox proportional hazards model, comparing the two groups of patients. Pathology Data Division is follow-up in progress.

MAJOR FINDINGS: Two hundred ninety-two cases have been completed. An additional 78 cases are close to completion. Pathology Data Division follow-up is in progress.

Preliminary analysis of 37 node-negative tumors, statistical analysis was performed. The Jonckheere-Terpstra test (Hollander & Wolfe, 1973) was used to determine if the chromosomal spot counts were identically distributed in each grade considered. In addition, the standardized Jonckheere-Terpstra test statistics allow one to determine the relationship between chromosomal spot counts and grade. Two-sided asymptotic p-values were determined. Integer values were used for each chromosomal spot count. The Jonchkheere-Terpstra test was also used to compare normal tissue chromosomal spot counts to tumor chromosomal spot counts, with both tissues coming from the same biopsy.

Comparison of the chromosomal profiles to the tumor grade as determined by the Bloom and Richardson methods modified by Elston

did not show any correlation. However, if the tumors were grouped according to the nuclear grade, there was a statistically significant increase in the copy numbers of chromosome 1 with nuclear grade. Similarly, increasing numbers of chromosome 18 were observed with increase in nuclear grade. However, there was no significant increase in the copy numbers of chromosomes 8, 11, 13/21, 17 and X when correlated with nuclear grade. All of them showed extra copies in nuclear grade I, II, and III tumors. Comparison of copy numbers of the different chromosomes in tumor to normal epithelial cells showed a gain for chromosomes 8, 11, 13/21, 17, and X. However, in individual cases, loss of chromosome 17 and X chromosome was encountered.

p53 analysis is in progress.